

SEQUENCE LISTING



<110> SHONE, Clifford Charles
SUTTON, John Mark
HALLIS, Bassam
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<120> Delivery of Superoxide Dismutase to Neuronal Cells

<130> 1581.0800000

<140> 09/831,050

<141> 1999-11-05

<150> PCT/GB99/03699

<151> 1998-11-05

<160> 14

<170> PatentIn Ver. 2.1

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<211> 204

<212> PRT

<213> Bacillus caldotenax

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Pro His Ile Asp Lys Glu Thr Met Asn Ile His His Thr Lys His His
20 25 30

Asn Thr Tyr Val Thr Asn Leu Asn Ala Ala Leu Glu Gly His Pro Asp
35 40 45

Leu Gln Asn Lys Ser Leu Glu Glu Leu Leu Ser Asn Leu Glu Ala Leu
50 55 60

Pro Glu Ser Ile Arg Thr Ala Val Arg Asn Asn Gly Gly Gly His Ala
65 70 75 80

Asn His Ser Leu Phe Trp Thr Ile Leu Ser Pro Asn Gly Gly Gly Glu
85 90 95

Pro Thr Gly Glu Leu Ala Glu Ala Ile Asn Lys Lys Phe Gly Ser Phe
100 105 110

Thr Ala Phe Lys Asp Glu Phe Ser Lys Ala Ala Ala Gly Arg Phe Gly
115 120 125

Ser Gly Trp Ala Trp Leu Val Val Asn Asn Gly Glu Leu Glu Ile Thr
130 135 140

Ser Thr Pro Asn Gln Asp Ser Pro Ile Met Glu Gly Lys Thr Pro Ile
145 150 155 160

Leu Gly Leu Asp Val Trp Glu His Ala Tyr Tyr Leu Lys Tyr Gln Asn
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Arg Arg Pro Glu Tyr Ile Ala Ala Phe Trp Asn Ile Val Asn Trp Asp
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Glu Val Ala Lys Arg Tyr Ser Glu Ala Lys Ala Lys
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<213> Bacillus stearothermophilus

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35 40 45
Leu Gln Asn Lys Ser Leu Glu Glu Leu Leu Ser Asn Leu Glu Ala Leu
50 55 60
Pro Glu Ser Ile Arg Thr Ala Val Arg Asn Asn Gly Gly Gly His Ala
65 70 75 80
Asn His Ser Leu Phe Trp Thr Ile Leu Ser Pro Asn Gly Gly Gly Glu
85 90 95
Pro Thr Gly Glu Leu Ala Asp Ala Ile Asn Lys Lys Phe Gly Ser Phe
100 105 110
Thr Ala Phe Lys Asp Glu Phe Ser Lys Ala Ala Ala Gly Arg Phe Gly
115 120 125
Ser Gly Trp Ala Trp Leu Val Val Asn Asn Gly Glu Leu Glu Ile Thr
130 135 140
Ser Thr Pro Asn Gln Asp Ser Pro Ile Met Glu Gly Lys Thr Pro Ile
145 150 155 160
Leu Gly Leu Asp Val Trp Glu His Ala Tyr Tyr Leu Lys Tyr Gln Asn
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Arg Arg Pro Glu Tyr Ile Ala Ala Phe Trp Asn Val Val Asn Trp Asp
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Glu Val Ala Lys Arg Tyr Ser Glu Ala Lys Ala Lys
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<210> 3
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:construct

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20 25 30
Asn Thr Tyr Val Thr Asn Leu Asn Ala Ala Leu Glu Gly His Pro Asp
35 40 45

Leu	Gln	Asn	Lys	Ser	Leu	Glu	Glu	Leu	Leu	Ser	Asn	Leu	Glu	Ala	Leu
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Pro	Glu	Ser	Ile	Arg	Thr	Ala	Val	Arg	Asn	Asn	Gly	Gly	Gly	His	Ala
65					70				75						80
Asn	His	Ser	Leu	Phe	Trp	Thr	Ile	Leu	Ser	Pro	Asn	Gly	Gly	Gly	Glu
				85					90					95	
Pro	Thr	Gly	Glu	Leu	Ala	Asp	Ala	Ile	Asn	Lys	Lys	Phe	Gly	Ser	Phe
			100					105					110		
Thr	Ala	Phe	Lys	Asp	Glu	Phe	Ser	Lys	Ala	Ala	Ala	Gly	Arg	Phe	Gly
		115					120					125			
Ser	Gly	Trp	Ala	Trp	Leu	Val	Val	Asn	Asn	Gly	Glu	Leu	Glu	Ile	Thr
	130					135					140				
Ser	Thr	Pro	Asn	Gln	Asp	Ser	Pro	Ile	Met	Glu	Gly	Lys	Thr	Pro	Ile
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Leu	Gly	Leu	Asp	Val	Trp	Glu	His	Ala	Tyr	Tyr	Leu	Lys	Tyr	Gln	Asn
				165					170					175	
Arg	Arg	Pro	Glu	Tyr	Ile	Ala	Ala	Phe	Trp	Asn	Val	Val	Asn	Trp	Asp
			180					185						190	
Glu	Val	Ala	Lys	Arg	Tyr	Ser	Glu	Ala	Lys	Ala	Lys	Gln	Arg	Ser	Cys
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Gly	Leu	Val	Pro	Arg	Gly	Ser	Gly	Pro	Gly	Ser	Ala	Leu	Asn	Asp	Leu
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Cys	Ile	Lys	Val	Asn	Asn	Trp	Asp	Leu	Phe	Phe	Ser	Pro	Ser	Glu	Asp
225					230					235					240
Asn	Phe	Thr	Asn	Asp	Leu	Asn	Lys	Gly	Glu	Glu	Ile	Thr	Ser	Asp	Thr
				245					250					255	
Asn	Ile	Glu	Ala	Ala	Glu	Glu	Asn	Ile	Ser	Leu	Asp	Leu	Ile	Gln	Gln
			260					265					270		
Tyr	Tyr	Leu	Thr	Phe	Asn	Phe	Asp	Asn	Glu	Pro	Glu	Asn	Ile	Ser	Ile
		275					280					285			
Glu	Asn	Leu	Ser	Ser	Asp	Ile	Ile	Gly	Gln	Leu	Glu	Leu	Met	Pro	Asn
	290					295					300				
Ile	Glu	Arg	Phe	Pro	Asn	Gly	Lys	Lys	Tyr	Glu	Leu	Asp	Lys	Tyr	Thr
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Met	Phe	His	Tyr	Leu	Arg	Ala	Gln	Glu	Phe	Glu	His	Gly	Lys	Ser	Arg
				325					330					335	
Ile	Ala	Leu	Thr	Asn	Ser	Val	Asn	Glu	Ala	Leu	Leu	Asn	Pro	Ser	Arg
			340					345					350		
Val	Tyr	Thr	Phe	Phe	Ser	Ser	Asp	Tyr	Val	Lys	Lys	Val	Asn	Lys	Ala
		355					360					365			
Thr	Glu	Ala	Ala	Met	Phe	Leu	Gly	Trp	Val	Glu	Gln	Leu	Val	Tyr	Asp
	370					375					380				
Phe	Thr	Asp	Glu	Thr	Ser	Glu	Val	Ser	Thr	Thr	Asp	Lys	Ile	Ala	Asp
385					390					395					400

Ile	Thr	Ile	Ile	Ile	Pro	Tyr	Ile	Gly	Pro	Ala	Leu	Asn	Ile	Gly	Asn	
				405					410					415		
Met	Leu	Tyr	Lys	Asp	Asp	Phe	Val	Gly	Ala	Leu	Ile	Phe	Ser	Gly	Ala	
			420					425					430			
Val	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Ile	Ala	Ile	Pro	Val	Leu	Gly	
		435					440					445				
Thr	Phe	Ala	Leu	Val	Ser	Tyr	Ile	Ala	Asn	Lys	Val	Leu	Thr	Val	Gln	
	450					455					460					
Thr	Ile	Asp	Asn	Ala	Leu	Ser	Lys	Arg	Asn	Glu	Lys	Trp	Asp	Glu	Val	
465					470					475					480	
Tyr	Lys	Tyr	Ile	Val	Thr	Asn	Trp	Leu	Ala	Lys	Val	Asn	Thr	Gln	Ile	
				485					490					495		
Asp	Leu	Ile	Arg	Lys	Lys	Met	Lys	Glu	Ala	Leu	Glu	Asn	Gln	Ala	Glu	
			500					505					510			
Ala	Thr	Lys	Ala	Ile	Ile	Asn	Tyr	Gln	Tyr	Asn	Gln	Tyr	Thr	Glu	Glu	
		515				520					525					
Glu	Lys	Asn	Asn	Ile	Asn	Phe	Asn	Ile	Asp	Asp	Leu	Ser	Ser	Lys	Leu	
	530					535					540					
Asn	Glu	Ser	Ile	Asn	Lys	Ala	Met	Ile	Asn	Ile	Asn	Lys	Phe	Leu	Asn	
545					550					555					560	
Gln	Cys	Ser	Val	Ser	Tyr	Leu	Met	Asn	Ser	Met	Ile	Pro	Tyr	Gly	Val	
				565					570					575		
Lys	Arg	Leu	Glu	Asp	Phe	Asp	Ala	Ser	Leu	Lys	Asp	Ala	Leu	Leu	Lys	
			580					585					590			
Tyr	Ile	Tyr	Asp	Asn	Arg	Gly	Thr	Leu	Ile	Gly	Gln	Val	Asp	Arg	Leu	
		595					600					605				
Lys	Asp	Lys	Val	Asn	Asn	Thr	Leu	Ser	Thr	Asp	Ile	Pro	Phe	Gln	Leu	
	610					615					620					
Ser	Lys	Tyr	Val	Asp	Asn	Gln	Arg	Leu	Leu	Ser	Thr	Phe	Thr	Glu	Tyr	
625					630					635					640	
Ile	Lys	Asn	Ile	Ile	Asn	Thr	Ser	Ile	Leu	Asn	Leu	Arg	Tyr	Glu	Ser	
				645					650					655		
Asn	His	Leu	Ile	Asp	Leu	Ser	Arg	Tyr	Ala	Ser	Lys	Ile	Asn	Ile	Gly	
		660						665					670			
Ser	Lys	Val	Asn	Phe	Asp	Pro	Ile	Asp	Lys	Asn	Gln	Ile	Gln	Leu	Phe	
		675					680					685				
Asn	Leu	Glu	Ser	Ser	Lys	Ile	Glu	Val	Ile	Leu	Lys	Asn	Ala	Ile	Val	
		690				695					700					
Tyr	Asn	Ser	Met	Tyr	Glu	Asn	Phe	Ser	Thr	Ser	Phe	Trp	Ile	Arg	Ile	
705					710					715					720	
Pro	Lys	Tyr	Phe	Asn	Ser	Ile	Ser	Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	
				725					730					735		
Asn	Cys	Met	Glu	Asn	Asn	Ser	Gly	Trp	Lys	Val	Ser	Leu	Asn	Tyr	Gly	
			740					745					750			

Glu	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Gln	Glu	Ile	Lys	Gln	Arg	Val		
		755					760					765					
Val	Phe	Lys	Tyr	Ser	Gln	Met	Ile	Asn	Ile	Ser	Asp	Tyr	Ile	Asn	Arg		
	770					775					780						
Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Asn	Asn	Ser	Lys	Ile		
785					790					795					800		
Tyr	Ile	Asn	Gly	Arg	Leu	Ile	Asp	Gln	Lys	Pro	Ile	Ser	Asn	Leu	Gly		
			805						810					815			
Asn	Ile	His	Ala	Ser	Asn	Asn	Ile	Met	Phe	Lys	Leu	Asp	Gly	Cys	Arg		
			820					825					830				
Asp	Thr	His	Arg	Tyr	Ile	Trp	Ile	Lys	Tyr	Phe	Asn	Leu	Phe	Asp	Lys		
		835					840					845					
Glu	Leu	Asn	Glu	Lys	Glu	Ile	Lys	Asp	Leu	Tyr	Asp	Asn	Gln	Ser	Asn		
	850					855					860						
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Pro	Tyr	Tyr	Met	Leu	Asn	Leu	Tyr	Asp	Pro	Asn	Lys	Tyr	Val	Asp	Val		
			885						890					895			
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		900						905					910				
Ser	Val	Met	Thr	Thr	Asn	Ile	Tyr	Leu	Asn	Ser	Ser	Leu	Tyr	Arg	Gly		
		915					920					925					
Thr	Lys	Phe	Ile	Ile	Lys	Lys	Tyr	Ala	Ser	Gly	Asn	Lys	Asp	Asn	Ile		
	930					935					940						
Val	Arg	Asn	Asn	Asp	Arg	Val	Tyr	Ile	Asn	Val	Val	Val	Lys	Asn	Lys		
945					950					955					960		
Glu	Tyr	Arg	Leu	Ala	Thr	Asn	Ala	Ser	Gln	Ala	Gly	Val	Glu	Lys	Ile		
			965						970				975				
Leu	Ser	Ala	Leu	Glu	Ile	Pro	Asp	Val	Gly	Asn	Leu	Ser	Gln	Val	Val		
		980						985					990				
Val	Met	Lys	Ser	Lys	Asn	Asp	Gln	Gly	Ile	Thr	Asn	Lys	Cys	Lys	Met		
	995					1000						1005					
Asn	Leu	Gln	Asp	Asn	Asn	Gly	Asn	Asp	Ile	Gly	Phe	Ile	Gly	Phe	His		
	1010					1015					1020						
Gln	Phe	Asn	Asn	Ile	Ala	Lys	Leu	Val	Ala	Ser	Asn	Trp	Tyr	Asn	Arg		
1025					1030					1035					1040		
Gln	Ile	Glu	Arg	Ser	Ser	Arg	Thr	Leu	Gly	Cys	Ser	Trp	Glu	Phe	Ile		
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<213> Artificial Sequence

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<223> Description of Artificial Sequence:construct

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          20          25          30

Asn  Thr  Tyr  Val  Thr  Asn  Leu  Asn  Ala  Ala  Leu  Glu  Gly  His  Pro  Asp
          35          40          45

Leu  Gln  Asn  Lys  Ser  Leu  Glu  Glu  Leu  Leu  Ser  Asn  Leu  Glu  Ala  Leu
          50          55          60

Pro  Glu  Ser  Ile  Arg  Thr  Ala  Val  Arg  Asn  Asn  Gly  Gly  Gly  His  Ala
 65          70          75          80

Asn  His  Ser  Leu  Phe  Trp  Thr  Ile  Leu  Ser  Pro  Asn  Gly  Gly  Gly  Glu
          85          90          95

Pro  Thr  Gly  Glu  Leu  Ala  Asp  Ala  Ile  Asn  Lys  Lys  Phe  Gly  Ser  Phe
          100          105          110

Thr  Ala  Phe  Lys  Asp  Glu  Phe  Ser  Lys  Ala  Ala  Ala  Gly  Arg  Phe  Gly
          115          120          125

Ser  Gly  Trp  Ala  Trp  Leu  Val  Val  Asn  Asn  Gly  Glu  Leu  Glu  Ile  Thr
 130          135          140

Ser  Thr  Pro  Asn  Gln  Asp  Ser  Pro  Ile  Met  Glu  Gly  Lys  Thr  Pro  Ile
 145          150          155          160

Leu  Gly  Leu  Asp  Val  Trp  Glu  His  Ala  Tyr  Tyr  Leu  Lys  Tyr  Gln  Asn
          165          170          175

Arg  Arg  Pro  Glu  Tyr  Ile  Ala  Ala  Phe  Trp  Asn  Val  Val  Asn  Trp  Asp
          180          185          190

Glu  Val  Ala  Lys  Arg  Tyr  Ser  Glu  Ala  Lys  Ala  Lys  Gln  Arg  Ser  Cys
          195          200          205

Gly  Leu  Val  Pro  Arg  Gly  Ser  Gly  Pro  Gly  Ser  Lys  Ala  Pro  Gly  Ile
 210          215          220

Cys  Ile  Asp  Val  Asp  Asn  Glu  Asp  Leu  Phe  Phe  Ile  Ala  Asp  Lys  Asn
 225          230          235          240

Ser  Phe  Ser  Asp  Asp  Leu  Ser  Lys  Asn  Glu  Arg  Ile  Glu  Tyr  Asn  Thr
          245          250          255

Gln  Ser  Asn  Tyr  Ile  Glu  Asn  Asp  Phe  Pro  Ile  Asn  Glu  Leu  Ile  Leu
          260          265          270

Asp  Thr  Asp  Leu  Ile  Ser  Lys  Ile  Glu  Leu  Pro  Ser  Glu  Asn  Thr  Glu
 275          280          285

Ser  Leu  Thr  Asp  Phe  Asn  Val  Asp  Val  Pro  Val  Tyr  Glu  Lys  Gln  Pro
 290          295          300

Ala  Ile  Lys  Lys  Ile  Phe  Thr  Asp  Glu  Asn  Thr  Ile  Phe  Gln  Tyr  Leu
 305          310          315          320

Tyr  Ser  Gln  Thr  Phe  Pro  Leu  Asp  Ile  Arg  Asp  Ile  Ser  Leu  Thr  Ser
          325          330          335

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Ser	Phe	Asp	Asp	Ala	Leu	Leu	Phe	Ser	Asn	Lys	Val	Tyr	Ser	Phe	Phe	
			340					345					350			
Ser	Met	Asp	Tyr	Ile	Lys	Thr	Ala	Asn	Lys	Val	Val	Glu	Ala	Gly	Leu	
		355					360					365				
Phe	Ala	Gly	Trp	Val	Lys	Gln	Ile	Val	Asn	Asp	Phe	Val	Ile	Glu	Ala	
	370					375					380					
Asn	Lys	Ser	Asn	Thr	Met	Asp	Lys	Ile	Ala	Asp	Ile	Ser	Leu	Ile	Val	
385					390					395					400	
Pro	Tyr	Ile	Gly	Leu	Ala	Leu	Asn	Val	Gly	Asn	Glu	Thr	Ala	Lys	Gly	
				405					410					415		
Asn	Phe	Glu	Asn	Ala	Phe	Glu	Ile	Ala	Gly	Ala	Ser	Ile	Leu	Leu	Glu	
			420					425					430			
Phe	Ile	Pro	Glu	Leu	Leu	Ile	Pro	Val	Val	Gly	Ala	Phe	Leu	Leu	Glu	
		435					440					445				
Ser	Tyr	Ile	Asp	Asn	Lys	Asn	Lys	Ile	Ile	Lys	Thr	Ile	Asp	Asn	Ala	
	450					455					460					
Leu	Thr	Lys	Arg	Asn	Glu	Lys	Trp	Ser	Asp	Met	Tyr	Gly	Leu	Ile	Val	
465					470					475					480	
Ala	Gln	Trp	Leu	Ser	Thr	Val	Asn	Thr	Gln	Phe	Tyr	Thr	Ile	Lys	Glu	
				485					490					495		
Gly	Met	Tyr	Lys	Ala	Leu	Asn	Tyr	Gln	Ala	Gln	Ala	Leu	Glu	Glu	Ile	
			500					505					510			
Ile	Lys	Tyr	Arg	Tyr	Asn	Ile	Tyr	Ser	Glu	Lys	Glu	Lys	Ser	Asn	Ile	
		515					520					525				
Asn	Ile	Asp	Phe	Asn	Asp	Ile	Asn	Ser	Lys	Leu	Asn	Glu	Gly	Ile	Asn	
	530					535					540					
Gln	Ala	Ile	Asp	Asn	Ile	Asn	Asn	Phe	Ile	Asn	Gly	Cys	Ser	Val	Ser	
545					550					555					560	
Tyr	Leu	Met	Lys	Lys	Met	Ile	Pro	Leu	Ala	Val	Glu	Lys	Leu	Leu	Asp	
				565					570					575		
Phe	Asp	Asn	Thr	Leu	Lys	Lys	Asn	Leu	Leu	Asn	Tyr	Ile	Asp	Glu	Asn	
			580				585						590			
Lys	Leu	Tyr	Leu	Ile	Gly	Ser	Ala	Glu	Tyr	Glu	Lys	Ser	Lys	Val	Asn	
		595					600					605				
Lys	Tyr	Leu	Lys	Thr	Ile	Met	Pro	Phe	Asp	Leu	Ser	Ile	Tyr	Thr	Asn	
	610					615					620					
Asp	Thr	Ile	Leu	Ile	Glu	Met	Phe	Asn	Lys	Tyr	Asn	Ser	Glu	Ile	Leu	
625					630					635					640	
Asn	Asn	Ile	Ile	Leu	Asn	Leu	Arg	Tyr	Lys	Asp	Asn	Asn	Leu	Ile	Asp	
				645					650					655		
Leu	Ser	Gly	Tyr	Gly	Ala	Lys	Val	Glu	Val	Tyr	Asp	Gly	Val	Glu	Leu	
			660					665					670			
Asn	Asp	Lys	Asn	Gln	Phe	Lys	Leu	Thr	Ser	Ser	Ala	Asn	Ser	Lys	Ile	
		675					680					685				

Arg	Val	Thr	Gln	Asn	Gln	Asn	Ile	Ile	Phe	Asn	Ser	Val	Phe	Leu	Asp	690	695	700
Phe	Ser	Val	Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Lys	Asn	Asp	Gly	705	710	715
Ile	Gln	Asn	Tyr	Ile	His	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Lys	725	730	735
Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Ile	Arg	Gly	Asn	Arg	Ile	Ile	Trp	740	745	750
Thr	Leu	Ile	Asp	Ile	Asn	Gly	Lys	Thr	Lys	Ser	Val	Phe	Phe	Glu	Tyr	755	760	765
Asn	Ile	Arg	Glu	Asp	Ile	Ser	Glu	Tyr	Ile	Asn	Arg	Trp	Phe	Phe	Val	770	775	780
Thr	Ile	Thr	Asn	Asn	Leu	Asn	Asn	Ala	Lys	Ile	Tyr	Ile	Asn	Gly	Lys	785	790	795
Leu	Glu	Ser	Asn	Thr	Asp	Ile	Lys	Asp	Ile	Arg	Glu	Val	Ile	Ala	Asn	805	810	815
Gly	Glu	Ile	Ile	Phe	Lys	Leu	Asp	Gly	Asp	Ile	Asp	Arg	Thr	Gln	Phe	820	825	830
Ile	Trp	Met	Lys	Tyr	Phe	Ser	Ile	Phe	Asn	Thr	Glu	Leu	Ser	Gln	Ser	835	840	845
Asn	Ile	Glu	Glu	Arg	Tyr	Lys	Ile	Gln	Ser	Tyr	Ser	Glu	Tyr	Leu	Lys	850	855	860
Asp	Phe	Trp	Gly	Asn	Pro	Leu	Met	Tyr	Asn	Lys	Glu	Tyr	Tyr	Met	Phe	865	870	875
Asn	Ala	Gly	Asn	Lys	Asn	Ser	Tyr	Ile	Lys	Leu	Lys	Lys	Asp	Ser	Pro	885	890	895
Val	Gly	Glu	Ile	Leu	Thr	Arg	Ser	Lys	Tyr	Asn	Gln	Asn	Ser	Lys	Tyr	900	905	910
Ile	Asn	Tyr	Arg	Asp	Leu	Tyr	Ile	Gly	Glu	Lys	Phe	Ile	Ile	Arg	Arg	915	920	925
Lys	Ser	Asn	Ser	Gln	Ser	Ile	Asn	Asp	Asp	Ile	Val	Arg	Lys	Glu	Asp	930	935	940
Tyr	Ile	Tyr	Leu	Asp	Phe	Phe	Asn	Leu	Asn	Gln	Glu	Trp	Arg	Val	Tyr	945	950	955
Thr	Tyr	Lys	Tyr	Phe	Lys	Lys	Glu	Glu	Glu	Lys	Leu	Phe	Leu	Ala	Pro	965	970	975
Ile	Ser	Asp	Ser	Asp	Glu	Phe	Tyr	Asn	Thr	Ile	Gln	Ile	Lys	Glu	Tyr	980	985	990
Asp	Glu	Gln	Pro	Thr	Tyr	Ser	Cys	Gln	Leu	Leu	Phe	Lys	Lys	Asp	Glu	995	1000	1005
Glu	Ser	Thr	Asp	Glu	Ile	Gly	Leu	Ile	Gly	Ile	His	Arg	Phe	Tyr	Glu	1010	1015	1020
Ser	Gly	Ile	Val	Phe	Glu	Glu	Tyr	Lys	Asp	Tyr	Phe	Cys	Ile	Ser	Lys	1025	1030	1035
																		1040

Trp Tyr Leu Lys Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly
1045 1050 1055

Cys Asn Trp Gln Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu
1060 1065 1070

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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:construct

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Asn Thr Tyr Val Thr Asn Leu Asn Ala Ala Leu Glu Gly His Pro Asp
35 40 45
Leu Gln Asn Lys Ser Leu Glu Glu Leu Leu Ser Asn Leu Glu Ala Leu
50 55 60
Pro Glu Ser Ile Arg Thr Ala Val Arg Asn Asn Gly Gly Gly His Ala
65 70 75 80
Asn His Ser Leu Phe Trp Thr Ile Leu Ser Pro Asn Gly Gly Gly Glu
85 90 95
Pro Thr Gly Glu Leu Ala Asp Ala Ile Asn Lys Lys Phe Gly Ser Phe
100 105 110
Thr Ala Phe Lys Asp Glu Phe Ser Lys Ala Ala Ala Gly Arg Phe Gly
115 120 125
Ser Gly Trp Ala Trp Leu Val Val Asn Asn Gly Glu Leu Glu Ile Thr
130 135 140
Ser Thr Pro Asn Gln Asp Ser Pro Ile Met Glu Gly Lys Thr Pro Ile
145 150 155 160
Leu Gly Leu Asp Val Trp Glu His Ala Tyr Tyr Leu Lys Tyr Gln Asn
165 170 175
Arg Arg Pro Glu Tyr Ile Ala Ala Phe Trp Asn Val Val Asn Trp Asp
180 185 190
Glu Val Ala Lys Arg Tyr Ser Glu Ala Lys Ala Lys Gln Arg Ser Cys
195 200 205
Gly Leu Val Pro Arg Gly Ser Gly Pro Gly Ser Lys Ala Pro Pro Arg
210 215 220
Leu Cys Ile Arg Val Asn Asn Arg Glu Leu Phe Phe Val Ala Ser Glu
225 230 235 240
Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro Lys Glu Ile Asp Asp
245 250 255
Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn Leu Asp Glu Val Ile

260					265					270					
Leu	Asp	Tyr	Asn	Ser	Glu	Thr	Ile	Pro	Gln	Ile	Ser	Asn	Gln	Thr	Leu
	275						280					285			
Asn	Thr	Leu	Val	Gln	Asp	Asp	Ser	Tyr	Val	Pro	Arg	Tyr	Asp	Ser	Asn
	290					295					300				
Gly	Thr	Ser	Glu	Ile	Glu	Glu	His	Asn	Val	Val	Asp	Leu	Asn	Val	Phe
	305					310					315				320
Phe	Tyr	Leu	His	Ala	Gln	Lys	Val	Pro	Glu	Gly	Glu	Thr	Asn	Ile	Ser
				325					330					335	
Leu	Thr	Ser	Ser	Ile	Asp	Thr	Ala	Leu	Ser	Glu	Glu	Ser	Gln	Val	Tyr
			340					345					350		
Thr	Phe	Phe	Ser	Ser	Glu	Phe	Ile	Asn	Thr	Ile	Asn	Lys	Pro	Val	His
		355					360					365			
Ala	Ala	Leu	Phe	Ile	Ser	Trp	Ile	Asn	Gln	Val	Ile	Arg	Asp	Phe	Thr
	370					375					380				
Thr	Glu	Ala	Thr	Gln	Lys	Ser	Thr	Phe	Asp	Lys	Ile	Ala	Asp	Ile	Ser
	385					390					395				400
Leu	Val	Val	Pro	Tyr	Val	Gly	Leu	Ala	Leu	Asn	Ile	Gly	Asn	Glu	Val
			405						410					415	
Gln	Lys	Glu	Asn	Phe	Lys	Glu	Ala	Phe	Glu	Leu	Leu	Gly	Ala	Gly	Ile
			420					425					430		
Leu	Leu	Glu	Phe	Val	Pro	Glu	Leu	Leu	Ile	Pro	Thr	Ile	Leu	Val	Phe
		435					440					445			
Thr	Ile	Lys	Ser	Phe	Ile	Gly	Ser	Ser	Glu	Asn	Lys	Asn	Lys	Ile	Ile
	450					455					460				
Lys	Ala	Ile	Asn	Asn	Ser	Leu	Met	Glu	Arg	Glu	Thr	Lys	Trp	Lys	Glu
	465					470					475				480
Ile	Tyr	Ser	Trp	Ile	Val	Ser	Asn	Trp	Leu	Thr	Arg	Ile	Asn	Thr	Gln
			485						490					495	
Phe	Asn	Lys	Arg	Lys	Glu	Gln	Met	Tyr	Gln	Ala	Leu	Gln	Asn	Gln	Val
			500					505					510		
Asp	Ala	Ile	Lys	Thr	Val	Ile	Glu	Tyr	Lys	Tyr	Asn	Asn	Tyr	Thr	Ser
		515					520					525			
Asp	Glu	Arg	Asn	Arg	Leu	Glu	Ser	Glu	Tyr	Asn	Ile	Asn	Asn	Ile	Arg
	530					535					540				
Glu	Glu	Leu	Asn	Lys	Lys	Val	Ser	Leu	Ala	Met	Glu	Asn	Ile	Glu	Arg
	545					550					555				560
Phe	Ile	Thr	Glu	Ser	Ser	Ile	Phe	Tyr	Leu	Met	Lys	Leu	Ile	Asn	Glu
			565						570					575	
Ala	Lys	Val	Ser	Lys	Leu	Arg	Glu	Tyr	Asp	Glu	Gly	Val	Lys	Glu	Tyr
			580					585					590		
Leu	Leu	Asp	Tyr	Ile	Ser	Glu	His	Arg	Ser	Ile	Leu	Gly	Asn	Ser	Val
		595					600					605			
Gln	Glu	Leu	Asn	Asp	Leu	Val	Thr	Ser	Thr	Leu	Asn	Asn	Ser	Ile	Pro

610					615					620					
Phe	Glu	Leu	Ser	Ser	Tyr	Thr	Asn	Asp	Lys	Ile	Leu	Ile	Leu	Tyr	Phe
625					630					635					640
Asn	Lys	Leu	Tyr	Lys	Lys	Ile	Lys	Asp	Asn	Ser	Ile	Leu	Asp	Met	Arg
				645					650					655	
Tyr	Glu	Asn	Asn	Lys	Phe	Ile	Asp	Ile	Ser	Gly	Tyr	Gly	Ser	Asn	Ile
			660					665					670		
Ser	Ile	Asn	Gly	Asp	Val	Tyr	Ile	Tyr	Ser	Thr	Asn	Arg	Asn	Gln	Phe
		675					680					685			
Gly	Ile	Tyr	Ser	Ser	Lys	Pro	Ser	Glu	Val	Asn	Ile	Ala	Gln	Asn	Asn
	690					695					700				
Asp	Ile	Ile	Tyr	Asn	Gly	Arg	Tyr	Gln	Asn	Phe	Ser	Ile	Ser	Phe	Trp
705					710					715					720
Val	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Lys	Val	Asn	Leu	Asn	Asn	Glu	Tyr
				725					730					735	
Thr	Ile	Ile	Asp	Cys	Ile	Arg	Asn	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser
			740					745					750		
Leu	Asn	Tyr	Asn	Lys	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Ala	Gly	Asn
		755					760					765			
Asn	Gln	Lys	Leu	Val	Phe	Asn	Tyr	Thr	Gln	Met	Ile	Ser	Ile	Ser	Asp
	770					775					780				
Tyr	Ile	Asn	Lys	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Gly
785					790					795					800
Asn	Ser	Arg	Ile	Tyr	Ile	Asn	Gly	Asn	Leu	Ile	Asp	Glu	Lys	Ser	Ile
			805						810					815	
Ser	Asn	Leu	Gly	Asp	Ile	His	Val	Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile
			820					825					830		
Val	Gly	Cys	Asn	Asp	Thr	Arg	Tyr	Val	Gly	Ile	Arg	Tyr	Phe	Lys	Val
		835					840					845			
Phe	Asp	Thr	Glu	Leu	Gly	Lys	Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asp
	850					855					860				
Glu	Pro	Asp	Pro	Ser	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu
865					870					875					880
Tyr	Asn	Lys	Arg	Tyr	Tyr	Leu	Leu	Asn	Leu	Leu	Arg	Thr	Asp	Lys	Ser
				885					890					895	
Ile	Thr	Gln	Asn	Ser	Asn	Phe	Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val
			900					905					910		
Tyr	Gln	Lys	Pro	Asn	Ile	Phe	Ser	Asn	Thr	Arg	Leu	Tyr	Thr	Gly	Val
		915					920					925			
Glu	Val	Ile	Ile	Arg	Lys	Asn	Gly	Ser	Thr	Asp	Ile	Ser	Asn	Thr	Asp
	930					935					940				
Asn	Phe	Val	Arg	Lys	Asn	Asp	Leu	Ala	Tyr	Ile	Asn	Val	Val	Asp	Arg
945					950					955					960
Asp	Val	Glu	Tyr	Arg	Leu	Tyr	Ala	Asp	Ile	Ser	Ile	Ala	Lys	Pro	Glu

965										970					975				
Lys	Ile	Ile	Lys	Leu	Ile	Arg	Thr	Ser	Asn	Ser	Asn	Asn	Ser	Leu	Gly				
			980					985					990						
Gln	Ile	Ile	Val	Met	Asp	Ser	Ile	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe				
			995				1000					1005							
Gln	Asn	Asn	Asn	Gly	Gly	Asn	Ile	Gly	Leu	Leu	Gly	Phe	His	Ser	Asn				
	1010					1015					1020								
Asn	Leu	Val	Ala	Ser	Ser	Trp	Tyr	Tyr	Asn	Asn	Ile	Arg	Lys	Asn	Thr				
	1025				1030						1035				1040				
Ser	Ser	Asn	Gly	Cys	Phe	Trp	Ser	Phe	Ile	Ser	Lys	Glu	His	Gly	Trp				
			1045					1050					1055						
Gln Glu Asn																			

<210> 6
 <211> 1092
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:construct

<400> 6

Met	Leu	Ser	Arg	Ala	Val	Cys	Gly	Thr	Ser	Arg	Gln	Leu	Ala	Pro	Ala
1				5					10					15	
Leu	Gly	Tyr	Leu	Gly	Ser	Arg	Gln	Lys	His	Ser	Arg	Gly	Ser	Pro	Ala
			20					25					30		
Leu	Pro	Tyr	Pro	Tyr	Asp	Ala	Leu	Glu	Pro	His	Ile	Asp	Lys	Glu	Thr
		35					40					45			
Met	Asn	Ile	His	His	Thr	Lys	His	His	Asn	Thr	Tyr	Val	Thr	Asn	Leu
	50					55					60				
Asn	Ala	Ala	Leu	Glu	Gly	His	Pro	Asp	Leu	Gln	Asn	Lys	Ser	Leu	Glu
	65				70					75					80
Glu	Leu	Leu	Ser	Asn	Leu	Glu	Ala	Leu	Pro	Glu	Ser	Ile	Arg	Thr	Ala
				85					90					95	
Val	Arg	Asn	Asn	Gly	Gly	Gly	His	Ala	Asn	His	Ser	Leu	Phe	Trp	Thr
			100					105					110		
Ile	Leu	Ser	Pro	Asn	Gly	Gly	Gly	Glu	Pro	Thr	Gly	Glu	Leu	Ala	Asp
		115				120						125			
Ala	Ile	Asn	Lys	Lys	Phe	Gly	Ser	Phe	Thr	Ala	Phe	Lys	Asp	Glu	Phe
	130					135					140				
Ser	Lys	Ala	Ala	Ala	Gly	Arg	Phe	Gly	Ser	Gly	Trp	Ala	Trp	Leu	Val
	145				150					155					160
Val	Asn	Asn	Gly	Glu	Leu	Glu	Ile	Thr	Ser	Thr	Pro	Asn	Gln	Asp	Ser
				165					170					175	
Pro	Ile	Met	Glu	Gly	Lys	Thr	Pro	Ile	Leu	Gly	Leu	Asp	Val	Trp	Glu
			180					185					190		

His	Ala	Tyr	Tyr	Leu	Lys	Tyr	Gln	Asn	Arg	Arg	Pro	Glu	Tyr	Ile	Ala		
		195					200					205					
Ala	Phe	Trp	Asn	Val	Val	Asn	Trp	Asp	Glu	Val	Ala	Lys	Arg	Tyr	Ser		
	210					215					220						
Glu	Ala	Lys	Ala	Lys	Gln	Arg	Ser	Cys	Gly	Leu	Val	Pro	Arg	Gly	Ser		
225					230					235					240		
Gly	Pro	Gly	Ser	Ala	Leu	Asn	Asp	Leu	Cys	Ile	Lys	Val	Asn	Asn	Trp		
				245					250					255			
Asp	Leu	Phe	Phe	Ser	Pro	Ser	Glu	Asp	Asn	Phe	Thr	Asn	Asp	Leu	Asn		
			260					265					270				
Lys	Gly	Glu	Glu	Ile	Thr	Ser	Asp	Thr	Asn	Ile	Glu	Ala	Ala	Glu	Glu		
		275					280					285					
Asn	Ile	Ser	Leu	Asp	Leu	Ile	Gln	Gln	Tyr	Tyr	Leu	Thr	Phe	Asn	Phe		
	290					295					300						
Asp	Asn	Glu	Pro	Glu	Asn	Ile	Ser	Ile	Glu	Asn	Leu	Ser	Ser	Asp	Ile		
305					310					315					320		
Ile	Gly	Gln	Leu	Glu	Leu	Met	Pro	Asn	Ile	Glu	Arg	Phe	Pro	Asn	Gly		
				325					330					335			
Lys	Lys	Tyr	Glu	Leu	Asp	Lys	Tyr	Thr	Met	Phe	His	Tyr	Leu	Arg	Ala		
			340					345					350				
Gln	Glu	Phe	Glu	His	Gly	Lys	Ser	Arg	Ile	Ala	Leu	Thr	Asn	Ser	Val		
		355					360					365					
Asn	Glu	Ala	Leu	Leu	Asn	Pro	Ser	Arg	Val	Tyr	Thr	Phe	Phe	Ser	Ser		
	370				375						380						
Asp	Tyr	Val	Lys	Lys	Val	Asn	Lys	Ala	Thr	Glu	Ala	Ala	Met	Phe	Leu		
385					390					395					400		
Gly	Trp	Val	Glu	Gln	Leu	Val	Tyr	Asp	Phe	Thr	Asp	Glu	Thr	Ser	Glu		
				405					410					415			
Val	Ser	Thr	Thr	Asp	Lys	Ile	Ala	Asp	Ile	Thr	Ile	Ile	Ile	Pro	Tyr		
			420					425					430				
Ile	Gly	Pro	Ala	Leu	Asn	Ile	Gly	Asn	Met	Leu	Tyr	Lys	Asp	Asp	Phe		
		435					440					445					
Val	Gly	Ala	Leu	Ile	Phe	Ser	Gly	Ala	Val	Ile	Leu	Leu	Glu	Phe	Ile		
	450					455					460						
Pro	Glu	Ile	Ala	Ile	Pro	Val	Leu	Gly	Thr	Phe	Ala	Leu	Val	Ser	Tyr		
465					470					475					480		
Ile	Ala	Asn	Lys	Val	Leu	Thr	Val	Gln	Thr	Ile	Asp	Asn	Ala	Leu	Ser		
				485					490					495			
Lys	Arg	Asn	Glu	Lys	Trp	Asp	Glu	Val	Tyr	Lys	Tyr	Ile	Val	Thr	Asn		
			500					505					510				
Trp	Leu	Ala	Lys	Val	Asn	Thr	Gln	Ile	Asp	Leu	Ile	Arg	Lys	Lys	Met		
		515					520					525					
Lys	Glu	Ala	Leu	Glu	Asn	Gln	Ala	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asn		
	530					535					540						

Tyr	Gln	Tyr	Asn	Gln	Tyr	Thr	Glu	Glu	Glu	Lys	Asn	Asn	Ile	Asn	Phe	545	550	555	560
Asn	Ile	Asp	Asp	Leu	Ser	Ser	Lys	Leu	Asn	Glu	Ser	Ile	Asn	Lys	Ala	565	570	575	
Met	Ile	Asn	Ile	Asn	Lys	Phe	Leu	Asn	Gln	Cys	Ser	Val	Ser	Tyr	Leu	580	585	590	
Met	Asn	Ser	Met	Ile	Pro	Tyr	Gly	Val	Lys	Arg	Leu	Glu	Asp	Phe	Asp	595	600	605	
Ala	Ser	Leu	Lys	Asp	Ala	Leu	Leu	Lys	Tyr	Ile	Tyr	Asp	Asn	Arg	Gly	610	615	620	
Thr	Leu	Ile	Gly	Gln	Val	Asp	Arg	Leu	Lys	Asp	Lys	Val	Asn	Asn	Thr	625	630	635	640
Leu	Ser	Thr	Asp	Ile	Pro	Phe	Gln	Leu	Ser	Lys	Tyr	Val	Asp	Asn	Gln	645	650	655	
Arg	Leu	Leu	Ser	Thr	Phe	Thr	Glu	Tyr	Ile	Lys	Asn	Ile	Ile	Asn	Thr	660	665	670	
Ser	Ile	Leu	Asn	Leu	Arg	Tyr	Glu	Ser	Asn	His	Leu	Ile	Asp	Leu	Ser	675	680	685	
Arg	Tyr	Ala	Ser	Lys	Ile	Asn	Ile	Gly	Ser	Lys	Val	Asn	Phe	Asp	Pro	690	695	700	
Ile	Asp	Lys	Asn	Gln	Ile	Gln	Leu	Phe	Asn	Leu	Glu	Ser	Ser	Lys	Ile	705	710	715	720
Glu	Val	Ile	Leu	Lys	Asn	Ala	Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	Asn	725	730	735	
Phe	Ser	Thr	Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Ser	Ile	740	745	750	
Ser	Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Glu	Asn	Asn	Ser	755	760	765	
Gly	Trp	Lys	Val	Ser	Leu	Asn	Tyr	Gly	Glu	Ile	Ile	Trp	Thr	Leu	Gln	770	775	780	
Asp	Thr	Gln	Glu	Ile	Lys	Gln	Arg	Val	Val	Phe	Lys	Tyr	Ser	Gln	Met	785	790	795	800
Ile	Asn	Ile	Ser	Asp	Tyr	Ile	Asn	Arg	Trp	Ile	Phe	Val	Thr	Ile	Thr	805	810	815	
Asn	Asn	Arg	Leu	Asn	Asn	Ser	Lys	Ile	Tyr	Ile	Asn	Gly	Arg	Leu	Ile	820	825	830	
Asp	Gln	Lys	Pro	Ile	Ser	Asn	Leu	Gly	Asn	Ile	His	Ala	Ser	Asn	Asn	835	840	845	
Ile	Met	Phe	Lys	Leu	Asp	Gly	Cys	Arg	Asp	Thr	His	Arg	Tyr	Ile	Trp	850	855	860	
Ile	Lys	Tyr	Phe	Asn	Leu	Phe	Asp	Lys	Glu	Leu	Asn	Glu	Lys	Glu	Ile	865	870	875	880
Lys	Asp	Leu	Tyr	Asp	Asn	Gln	Ser	Asn	Ser	Gly	Ile	Leu	Lys	Asp	Phe	885	890	895	

Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu
900 905 910

Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly
915 920 925

Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile
930 935 940

Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys
945 950 955 960

Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val
965 970 975

Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn
980 985 990

Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro
995 1000 1005

Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp
1010 1015 1020

Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly
1025 1030 1035 1040

Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys
1045 1050 1055

Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg
1060 1065 1070

Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly
1075 1080 1085

Glu Arg Pro Leu
1090

<210> 7

<211> 1095

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:construct

<400> 7

Met Leu Ser Arg Ala Val Cys Gly Thr Ser Arg Gln Leu Ala Pro Ala
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Leu Gly Tyr Leu Gly Ser Arg Gln Lys His Ser Arg Gly Ser Pro Ala
20 25 30

Leu Pro Tyr Pro Tyr Asp Ala Leu Glu Pro His Ile Asp Lys Glu Thr
35 40 45

Met Asn Ile His His Thr Lys His His Asn Thr Tyr Val Thr Asn Leu
50 55 60

Asn Ala Ala Leu Glu Gly His Pro Asp Leu Gln Asn Lys Ser Leu Glu
65 70 75 80

Glu Leu Leu Ser Asn Leu Glu Ala Leu Pro Glu Ser Ile Arg Thr Ala

85										90					95						
Val	Arg	Asn	Asn	Gly	Gly	Gly	His	Ala	Asn	His	Ser	Leu	Phe	Trp	Thr						
			100					105					110								
Ile	Leu	Ser	Pro	Asn	Gly	Gly	Gly	Glu	Pro	Thr	Gly	Glu	Leu	Ala	Asp						
		115					120					125									
Ala	Ile	Asn	Lys	Lys	Phe	Gly	Ser	Phe	Thr	Ala	Phe	Lys	Asp	Glu	Phe						
	130					135					140										
Ser	Lys	Ala	Ala	Ala	Gly	Arg	Phe	Gly	Ser	Gly	Trp	Ala	Trp	Leu	Val						
145					150					155					160						
Val	Asn	Asn	Gly	Glu	Leu	Glu	Ile	Thr	Ser	Thr	Pro	Asn	Gln	Asp	Ser						
			165						170					175							
Pro	Ile	Met	Glu	Gly	Lys	Thr	Pro	Ile	Leu	Gly	Leu	Asp	Val	Trp	Glu						
			180					185					190								
His	Ala	Tyr	Tyr	Leu	Lys	Tyr	Gln	Asn	Arg	Arg	Pro	Glu	Tyr	Ile	Ala						
		195					200					205									
Ala	Phe	Trp	Asn	Val	Val	Asn	Trp	Asp	Glu	Val	Ala	Lys	Arg	Tyr	Ser						
	210					215					220										
Glu	Ala	Lys	Ala	Lys	Gln	Arg	Ser	Cys	Gly	Leu	Val	Pro	Arg	Gly	Ser						
225					230					235					240						
Gly	Pro	Gly	Ser	Lys	Ala	Pro	Gly	Ile	Cys	Ile	Asp	Val	Asp	Asn	Glu						
			245					250						255							
Asp	Leu	Phe	Phe	Ile	Ala	Asp	Lys	Asn	Ser	Phe	Ser	Asp	Asp	Leu	Ser						
		260					265						270								
Lys	Asn	Glu	Arg	Ile	Glu	Tyr	Asn	Thr	Gln	Ser	Asn	Tyr	Ile	Glu	Asn						
	275						280					285									
Asp	Phe	Pro	Ile	Asn	Glu	Leu	Ile	Leu	Asp	Thr	Asp	Leu	Ile	Ser	Lys						
	290				295						300										
Ile	Glu	Leu	Pro	Ser	Glu	Asn	Thr	Glu	Ser	Leu	Thr	Asp	Phe	Asn	Val						
305					310					315					320						
Asp	Val	Pro	Val	Tyr	Glu	Lys	Gln	Pro	Ala	Ile	Lys	Lys	Ile	Phe	Thr						
			325					330						335							
Asp	Glu	Asn	Thr	Ile	Phe	Gln	Tyr	Leu	Tyr	Ser	Gln	Thr	Phe	Pro	Leu						
		340					345						350								
Asp	Ile	Arg	Asp	Ile	Ser	Leu	Thr	Ser	Ser	Phe	Asp	Asp	Ala	Leu	Leu						
	355					360					365										
Phe	Ser	Asn	Lys	Val	Tyr	Ser	Phe	Phe	Ser	Met	Asp	Tyr	Ile	Lys	Thr						
	370					375					380										
Ala	Asn	Lys	Val	Val	Glu	Ala	Gly	Leu	Phe	Ala	Gly	Trp	Val	Lys	Gln						
385					390					395					400						
Ile	Val	Asn	Asp	Phe	Val	Ile	Glu	Ala	Asn	Lys	Ser	Asn	Thr	Met	Asp						
			405					410						415							
Lys	Ile	Ala	Asp	Ile	Ser	Leu	Ile	Val	Pro	Tyr	Ile	Gly	Leu	Ala	Leu						
		420					425					430									
Asn	Val	Gly	Asn	Glu	Thr	Ala	Lys	Gly	Asn	Phe	Glu	Asn	Ala	Phe	Glu						

435					440					445					
Ile	Ala	Gly	Ala	Ser	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Leu	Leu	Ile
450					455					460					
Pro	Val	Val	Gly	Ala	Phe	Leu	Leu	Glu	Ser	Tyr	Ile	Asp	Asn	Lys	Asn
465					470					475					480
Lys	Ile	Ile	Lys	Thr	Ile	Asp	Asn	Ala	Leu	Thr	Lys	Arg	Asn	Glu	Lys
				485					490					495	
Trp	Ser	Asp	Met	Tyr	Gly	Leu	Ile	Val	Ala	Gln	Trp	Leu	Ser	Thr	Val
			500					505					510		
Asn	Thr	Gln	Phe	Tyr	Thr	Ile	Lys	Glu	Gly	Met	Tyr	Lys	Ala	Leu	Asn
		515					520					525			
Tyr	Gln	Ala	Gln	Ala	Leu	Glu	Glu	Ile	Ile	Lys	Tyr	Arg	Tyr	Asn	Ile
	530					535					540				
Tyr	Ser	Glu	Lys	Glu	Lys	Ser	Asn	Ile	Asn	Ile	Asp	Phe	Asn	Asp	Ile
545						550					555				560
Asn	Ser	Lys	Leu	Asn	Glu	Gly	Ile	Asn	Gln	Ala	Ile	Asp	Asn	Ile	Asn
				565					570					575	
Asn	Phe	Ile	Asn	Gly	Cys	Ser	Val	Ser	Tyr	Leu	Met	Lys	Lys	Met	Ile
			580					585						590	
Pro	Leu	Ala	Val	Glu	Lys	Leu	Leu	Asp	Phe	Asp	Asn	Thr	Leu	Lys	Lys
		595				600						605			
Asn	Leu	Leu	Asn	Tyr	Ile	Asp	Glu	Asn	Lys	Leu	Tyr	Leu	Ile	Gly	Ser
	610					615					620				
Ala	Glu	Tyr	Glu	Lys	Ser	Lys	Val	Asn	Lys	Tyr	Leu	Lys	Thr	Ile	Met
625						630					635				640
Pro	Phe	Asp	Leu	Ser	Ile	Tyr	Thr	Asn	Asp	Thr	Ile	Leu	Ile	Glu	Met
				645					650					655	
Phe	Asn	Lys	Tyr	Asn	Ser	Glu	Ile	Leu	Asn	Asn	Ile	Ile	Leu	Asn	Leu
				660				665					670		
Arg	Tyr	Lys	Asp	Asn	Asn	Leu	Ile	Asp	Leu	Ser	Gly	Tyr	Gly	Ala	Lys
		675					680					685			
Val	Glu	Val	Tyr	Asp	Gly	Val	Glu	Leu	Asn	Asp	Lys	Asn	Gln	Phe	Lys
	690					695					700				
Leu	Thr	Ser	Ser	Ala	Asn	Ser	Lys	Ile	Arg	Val	Thr	Gln	Asn	Gln	Asn
705						710					715				720
Ile	Ile	Phe	Asn	Ser	Val	Phe	Leu	Asp	Phe	Ser	Val	Ser	Phe	Trp	Ile
				725					730					735	
Arg	Ile	Pro	Lys	Tyr	Lys	Asn	Asp	Gly	Ile	Gln	Asn	Tyr	Ile	His	Asn
			740					745					750		
Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Lys	Asn	Asn	Ser	Gly	Trp	Lys	Ile
		755					760					765			
Ser	Ile	Arg	Gly	Asn	Arg	Ile	Ile	Trp	Thr	Leu	Ile	Asp	Ile	Asn	Gly
	770					775					780				
Lys	Thr	Lys	Ser	Val	Phe	Phe	Glu	Tyr	Asn	Ile	Arg	Glu	Asp	Ile	Ser

785		790		795		800
Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn Asn Leu Asn						
		805		810		815
Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp Ile						
		820		825		830
Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys Leu						
		835		840		845
Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe Ser						
		850		855		860
Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr Lys						
		865		870		875
Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro Leu						
		885		890		895
Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn Ser						
		900		905		910
Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Thr Arg						
		915		920		925
Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu Tyr						
		930		935		940
Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser Ile						
		945		950		955
Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe Phe						
		965		970		975
Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys Lys						
		980		985		990
Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu Phe						
		995		1000		1005
Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr Ser						
		1010		1015		1020
Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile Gly						
		1025		1030		1035
Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu Glu						
		1045		1050		1055
Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val Lys						
		1060		1065		1070
Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile Pro						
		1075		1080		1085
Lys Asp Glu Gly Trp Thr Glu						
		1090		1095		

<210> 8

<211> 1084

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:construct

<400> 8

Met Leu Ser Arg Ala Val Cys Gly Thr Ser Arg Gln Leu Ala Pro Ala
1 5 10 15

Leu Gly Tyr Leu Gly Ser Arg Gln Lys His Ser Arg Gly Ser Pro Ala
20 25 30

Leu Pro Tyr Pro Tyr Asp Ala Leu Glu Pro His Ile Asp Lys Glu Thr

Met Asn Ile His His Thr Lys His His Asn Thr Tyr Val Thr Asn Leu
50 55 60

Asn Ala Ala Leu Glu Gly His Pro Asp Leu Gln Asn Lys Ser Leu Glu
65 70 75 80

Glu Leu Leu Ser Asn Leu Glu Ala Leu Pro Glu Ser Ile Arg Thr Ala
85 90 95

Val Arg Asn Asn Gly Gly Gly His Ala Asn His Ser Leu Phe Trp Thr
100 105 110

Ile Leu Ser Pro Asn Gly Gly Gly Glu Pro Thr Gly Glu Leu Ala Asp
115 120 125

Ala Ile Asn Lys Lys Phe Gly Ser Phe Thr Ala Phe Lys Asp Glu Phe
130 135 140

Ser Lys Ala Ala Ala Gly Arg Phe Gly Ser Gly Trp Ala Trp Leu Val
145 150 155 160

Val Asn Asn Gly Glu Leu Glu Ile Thr Ser Thr Pro Asn Gln Asp Ser
165 170 175

Pro Ile Met Glu Gly Lys Thr Pro Ile Leu Gly Leu Asp Val Trp Glu
180 185 190

His Ala Tyr Tyr Leu Lys Tyr Gln Asn Arg Arg Pro Glu Tyr Ile Ala
195 200 205

Ala Phe Trp Asn Val Val Asn Trp Asp Glu Val Ala Lys Arg Tyr Ser
210 215 220

Glu Ala Lys Ala Lys Gln Arg Ser Cys Gly Leu Val Pro Arg Gly Ser
225 230 235 240

Gly Pro Gly Ser Lys Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn
245 250 255

Arg Glu Leu Phe Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp
260 265 270

Ile Asn Thr Pro Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Asn
275 280 285

Tyr Arg Asn Asn Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Glu Thr
290 295 300

Ile Pro Gln Ile Ser Asn Gln Thr Leu Asn Thr Leu Val Gln Asp Asp
305 310 315 320

Ser Tyr Val Pro Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu
325 330 335

His	Asn	Val	Val	Asp	Leu	Asn	Val	Phe	Phe	Tyr	Leu	His	Ala	Gln	Lys	
			340					345					350			
Val	Pro	Glu	Gly	Glu	Thr	Asn	Ile	Ser	Leu	Thr	Ser	Ser	Ile	Asp	Thr	
		355					360					365				
Ala	Leu	Ser	Glu	Glu	Ser	Gln	Val	Tyr	Thr	Phe	Phe	Ser	Ser	Glu	Phe	
	370					375					380					
Ile	Asn	Thr	Ile	Asn	Lys	Pro	Val	His	Ala	Ala	Leu	Phe	Ile	Ser	Trp	
385					390				395						400	
Ile	Asn	Gln	Val	Ile	Arg	Asp	Phe	Thr	Thr	Glu	Ala	Thr	Gln	Lys	Ser	
			405						410					415		
Thr	Phe	Asp	Lys	Ile	Ala	Asp	Ile	Ser	Leu	Val	Val	Pro	Tyr	Val	Gly	
			420					425					430			
Leu	Ala	Leu	Asn	Ile	Gly	Asn	Glu	Val	Gln	Lys	Glu	Asn	Phe	Lys	Glu	
		435					440					445				
Ala	Phe	Glu	Leu	Leu	Gly	Ala	Gly	Ile	Leu	Leu	Glu	Phe	Val	Pro	Glu	
	450					455					460					
Leu	Leu	Ile	Pro	Thr	Ile	Leu	Val	Phe	Thr	Ile	Lys	Ser	Phe	Ile	Gly	
465					470					475					480	
Ser	Ser	Glu	Asn	Lys	Asn	Lys	Ile	Ile	Lys	Ala	Ile	Asn	Asn	Ser	Leu	
				485					490					495		
Met	Glu	Arg	Glu	Thr	Lys	Trp	Lys	Glu	Ile	Tyr	Ser	Trp	Ile	Val	Ser	
			500					505					510			
Asn	Trp	Leu	Thr	Arg	Ile	Asn	Thr	Gln	Phe	Asn	Lys	Arg	Lys	Glu	Gln	
		515					520					525				
Met	Tyr	Gln	Ala	Leu	Gln	Asn	Gln	Val	Asp	Ala	Ile	Lys	Thr	Val	Ile	
	530					535					540					
Glu	Tyr	Lys	Tyr	Asn	Asn	Tyr	Thr	Ser	Asp	Glu	Arg	Asn	Arg	Leu	Glu	
545					550					555					560	
Ser	Glu	Tyr	Asn	Ile	Asn	Asn	Ile	Arg	Glu	Glu	Leu	Asn	Lys	Lys	Val	
				565					570					575		
Ser	Leu	Ala	Met	Glu	Asn	Ile	Glu	Arg	Phe	Ile	Thr	Glu	Ser	Ser	Ile	
			580					585					590			
Phe	Tyr	Leu	Met	Lys	Leu	Ile	Asn	Glu	Ala	Lys	Val	Ser	Lys	Leu	Arg	
		595					600						605			
Glu	Tyr	Asp	Glu	Gly	Val	Lys	Glu	Tyr	Leu	Leu	Asp	Tyr	Ile	Ser	Glu	
	610					615					620					
His	Arg	Ser	Ile	Leu	Gly	Asn	Ser	Val	Gln	Glu	Leu	Asn	Asp	Leu	Val	
625					630					635					640	
Thr	Ser	Thr	Leu	Asn	Asn	Ser	Ile	Pro	Phe	Glu	Leu	Ser	Ser	Tyr	Thr	
				645					650					655		
Asn	Asp	Lys	Ile	Leu	Ile	Leu	Tyr	Phe	Asn	Lys	Leu	Tyr	Lys	Lys	Ile	
			660					665					670			
Lys	Asp	Asn	Ser	Ile	Leu	Asp	Met	Arg	Tyr	Glu	Asn	Asn	Lys	Phe	Ile	
		675					680					685				

Asp	Ile	Ser	Gly	Tyr	Gly	Ser	Asn	Ile	Ser	Ile	Asn	Gly	Asp	Val	Tyr		
690						695					700						
Ile	Tyr	Ser	Thr	Asn	Arg	Asn	Gln	Phe	Gly	Ile	Tyr	Ser	Ser	Lys	Pro		
705					710					715					720		
Ser	Glu	Val	Asn	Ile	Ala	Gln	Asn	Asn	Asp	Ile	Ile	Tyr	Asn	Gly	Arg		
				725					730					735			
Tyr	Gln	Asn	Phe	Ser	Ile	Ser	Phe	Trp	Val	Arg	Ile	Pro	Lys	Tyr	Phe		
			740					745					750				
Asn	Lys	Val	Asn	Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asp	Cys	Ile	Arg		
		755					760					765					
Asn	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Leu	Asn	Tyr	Asn	Lys	Ile	Ile		
		770				775					780						
Trp	Thr	Leu	Gln	Asp	Thr	Ala	Gly	Asn	Asn	Gln	Lys	Leu	Val	Phe	Asn		
785					790					795					800		
Tyr	Thr	Gln	Met	Ile	Ser	Ile	Ser	Asp	Tyr	Ile	Asn	Lys	Trp	Ile	Phe		
				805					810					815			
Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Gly	Asn	Ser	Arg	Ile	Tyr	Ile	Asn		
			820					825					830				
Gly	Asn	Leu	Ile	Asp	Glu	Lys	Ser	Ile	Ser	Asn	Leu	Gly	Asp	Ile	His		
		835					840					845					
Val	Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile	Val	Gly	Cys	Asn	Asp	Thr	Arg		
		850				855					860						
Tyr	Val	Gly	Ile	Arg	Tyr	Phe	Lys	Val	Phe	Asp	Thr	Glu	Leu	Gly	Lys		
865					870					875					880		
Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asp	Glu	Pro	Asp	Pro	Ser	Ile	Leu		
				885					890					895			
Lys	Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr	Asn	Lys	Arg	Tyr	Tyr	Leu		
			900					905					910				
Leu	Asn	Leu	Leu	Arg	Thr	Asp	Lys	Ser	Ile	Thr	Gln	Asn	Ser	Asn	Phe		
		915					920					925					
Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val	Tyr	Gln	Lys	Pro	Asn	Ile	Phe		
		930				935					940						
Ser	Asn	Thr	Arg	Leu	Tyr	Thr	Gly	Val	Glu	Val	Ile	Ile	Arg	Lys	Asn		
945					950					955					960		
Gly	Ser	Thr	Asp	Ile	Ser	Asn	Thr	Asp	Asn	Phe	Val	Arg	Lys	Asn	Asp		
				965					970					975			
Leu	Ala	Tyr	Ile	Asn	Val	Val	Asp	Arg	Asp	Val	Glu	Tyr	Arg	Leu	Tyr		
			980					985					990				
Ala	Asp	Ile	Ser	Ile	Ala	Lys	Pro	Glu	Lys	Ile	Ile	Lys	Leu	Ile	Arg		
		995					1000					1005					
Thr	Ser	Asn	Ser	Asn	Asn	Ser	Leu	Gly	Gln	Ile	Ile	Val	Met	Asp	Ser		
		1010				1015						1020					
Ile	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe	Gln	Asn	Asn	Asn	Gly	Gly	Asn		
1025					1030					1035					1040		

Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val Ala Ser Ser Trp
1045 1050 1055

Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn Gly Cys Phe Trp
1060 1065 1070

Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
1075 1080

<210> 9

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide
comprising a mitochondrial leader from human MnSOD
and B. Stearothermophilus SOS

<400> 9

Met Leu Ser Arg Ala Val Cys Gly Thr Ser Arg Gln Leu Ala Pro Ala
1 5 10 15

Leu Gly Tyr Leu Gly Ser Arg Gln Lys His Ser Arg Gly Ser Pro Ala
20 25 30

Leu Pro Tyr Pro Tyr Asp Ala Leu Glu Pro His Ile Asp Lys Glu Thr
35 40 45

Met Asn Ile His His Thr Lys His His Asn Thr Tyr Val Thr Asn Leu
50 55 60

Asn Ala Ala Leu Glu Gly His Pro Asp Leu Gln Asn Lys Ser Leu Glu
65 70 75 80

Glu Leu Leu Ser Asn Leu Glu Ala Leu Pro Glu Ser Ile Arg Thr Ala
85 90 95

Val Arg Asn Asn Gly Gly Gly His Ala Asn His Ser Leu Phe Trp Thr
100 105 110

Ile Leu Ser Pro Asn Gly Gly Gly Glu Pro Thr Gly Glu Leu Ala Asp
115 120 125

Ala Ile Asn Lys Lys Phe Gly Ser Phe Thr Ala Phe Lys Asp Glu Phe
130 135 140

Ser Lys Ala Ala Ala Gly Arg Phe Gly Ser Gly Trp Ala Trp Leu Val
145 150 155 160

Val Asn Asn Gly Glu Leu Glu Ile Thr Ser Thr Pro Asn Gln Asp Ser
165 170 175

Pro Ile Met Glu Gly Lys Thr Pro Ile Leu Gly Leu Asp Val Trp Glu
180 185 190

His Ala Tyr Tyr Leu Lys Tyr Gln Asn Arg Arg Pro Glu Tyr Ile Ala
195 200 205

Ala Phe Trp Asn Val Val Asn Trp Asp Glu Val Ala Lys Arg Tyr Ser
210 215 220

Glu Ala Lys Ala Lys
225

<210> 10
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified human
mitochondrial leader sequence

<400> 10
Met Leu Ser Arg Ala Val Ser Gly Thr Ser Arg Gln Leu Ala Pro Ala
1 5 10 15
Leu Gly Tyr Leu Gly Ser Arg Gln
20

<210> 11
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified human
mitochondrial leader sequence

<400> 11
Met Leu Ser Arg Ala Val Cys Gly Thr Ser Arg Gln Leu Ala Pro Ala
1 5 10 15
Leu Gly Tyr Leu Gly Ser Arg Gln
20

<210> 12
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: linker peptide

<400> 12
Cys Gly Leu Val Pro Ala Gly Ser Gly Pro
1 5 10

<210> 13
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified human
mitochondrial leader sequence

<400> 13
Met Leu Ser Arg Ala Val Cys Gly Thr Ser Arg Gln Leu Ala Pro Ala
1 5 10 15
Leu Gly Tyr Leu Gly Ser Arg Gln Lys His Ser
20 25

<210> 14

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified human
mitochondrial leader sequence

<400> 14

Met	Leu	Ser	Arg	Ala	Val	Ser	Gly	Thr	Ser	Arg	Gln	Leu	Ala	Pro	Ala
1				5				10					15		

Leu	Gly	Tyr	Leu	Gly	Ser	Arg	Gln	Lys	His	Ser
			20					25		